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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/766,396

DATE: 06/26/2001  
TIME: 15:11:59

Input Set : N:\Crf3\RULE60\09766396.txt  
Output Set: N:\CRF3\06262001\I766396.raw

## SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:  
 6 (i) APPLICANT: Sutcliffe, Gregor J.  
 7 de Lecea, Luis  
 8 Siggins, George R.  
 9 Henriksen, Steven J.  
 11 (ii) TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,  
 12 COMPOSITIONS AND METHODS  
 14 (iii) NUMBER OF SEQUENCES: 26  
 16 (iv) CORRESPONDENCE ADDRESS:  
 17 (A) ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
 18 (B) STREET: 10666 North Torrey Pines Road, TPC-8  
 19 (C) CITY: La Jolla  
 20 (D) STATE: California  
 21 (E) COUNTRY: US  
 22 (F) ZIP: 92037  
 24 (v) COMPUTER READABLE FORM:  
 25 (A) MEDIUM TYPE: Floppy disk  
 26 (B) COMPUTER: IBM PC compatible  
 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 30 (vi) CURRENT APPLICATION DATA:  
 C--> 31 (A) APPLICATION NUMBER: US/09/766,396  
 C--> 32 (B) FILING DATE: 18-Jan-2001  
 33 (C) CLASSIFICATION:  
 35 (vii) PRIOR APPLICATION DATA:  
 36 (A) APPLICATION NUMBER: 08/857,389  
 37 (B) FILING DATE:  
 41 (viii) ATTORNEY/AGENT INFORMATION:  
 42 (A) NAME: Schmonsees, William  
 43 (B) REGISTRATION NUMBER: 31,796  
 44 (C) REFERENCE/DOCKET NUMBER: 22908-0002  
 46 (ix) TELECOMMUNICATION INFORMATION:  
 47 (A) TELEPHONE: (415) 324-7041  
 48 (B) TELEFAX: (415) 324-0638  
 51 (2) INFORMATION FOR SEQ ID NO: 1:  
 53 (i) SEQUENCE CHARACTERISTICS:  
 54 (A) LENGTH: 438 base pairs  
 55 (B) TYPE: nucleic acid  
 56 (C) STRANDEDNESS: single  
 57 (D) TOPOLOGY: linear  
 59 (ii) MOLECULE TYPE: cDNA  
 61 (iii) HYPOTHETICAL: NO  
 63 (iv) ANTI-SENSE: NO  
 65 (ix) FEATURE:  
 66 (A) NAME/KEY: CDS  
 67 (B) LOCATION: 30..368

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70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
72 AAAGCACAGA CTTCAGGTTT CCAAGGAGG ATG GGT GGC TGC AGC ACA AGA GGC 53  
73 Met Gly Gly Cys Ser Thr Arg Gly  
74 1 5  
76 AAG CGG CCG TCA GCC CTC AGT CTG CTG CTG CTG CTC TCG GGG 101  
77 Lys Arg Pro Ser Ala Leu Ser Leu Leu Leu Leu Leu Ser Gly  
78 10 15 20  
80 ATC GCA GCC TCT GCC CTC CCC CTG GAG AGC GGT CCC ACC GGC CAG GAC 149  
81 Ile Ala Ala Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp  
82 25 30 35 40  
84 AGT GTG CAG GAT GCC ACA GGC GGG AGG AGG ACC GGC CTT CTG ACT TTC 197  
85 Ser Val Gln Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe  
86 45 50 55  
88 CTT GCC TGG TGG CAT GAG TGG GCT TCC CAA GAC AGC TCC AGC ACC GCT 245  
89 Leu Ala Trp Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala  
90 60 65 70  
92 TTC GAA GGG GGT ACC CCG GAG CTG TCT AAG CGG CAG GAA AGA CCA CCC 293  
93 Phe Glu Gly Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro  
94 75 80 85  
96 CTC CAG CAG CCC CCA CAC CGG GAT AAA AAG CCC TGC AAG AAC TTC TTC 341  
97 Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe  
98 90 95 100  
100 TGG AAA ACC TTC TCC TCG TGC AAG TAGCCCGAGC CTGACCGGAG CCTGACCGGC 395  
101 Trp Lys Thr Phe Ser Ser Cys Lys  
102 105 110  
104 CACCCTGTGA ATGCAGCCGT GGCCTGAATA AAGAGTGTCA AGT 438  
107 (2) INFORMATION FOR SEQ ID NO: 2:  
109 (i) SEQUENCE CHARACTERISTICS:  
110 (A) LENGTH: 112 amino acids  
111 (B) TYPE: amino acid  
112 (D) TOPOLOGY: linear  
114 (ii) MOLECULE TYPE: protein  
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
117 Met Gly Cys Ser Thr Arg Gly Lys Arg Pro Ser Ala Leu Ser Leu  
118 1 5 10 15  
120 Leu Leu Leu Leu Leu Ser Gly Ile Ala Ala Ser Ala Leu Pro Leu  
121 20 25 30  
123 Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln Asp Ala Thr Gly Gly  
124 35 40 45  
126 Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala  
127 50 55 60  
129 Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly Thr Pro Glu Leu  
130 65 70 75 80  
132 Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp  
133 85 90 95  
135 Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
136 100 105 110  
142 (2) INFORMATION FOR SEQ ID NO: 3:  
144 (i) SEQUENCE CHARACTERISTICS:

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145 (A) LENGTH: 110 amino acids  
146 (B) TYPE: amino acid  
147 (D) TOPOLOGY: linear  
149 (ii) MOLECULE TYPE: protein  
151 (v) FRAGMENT TYPE: C-terminal  
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
157 Gln Cys Ala Leu Ala Ala Leu Cys Ile Val Leu Ala Leu Gly Gly Val  
158 1 5 10 15  
160 Thr Gly Ala Pro Ser Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser  
161 20 25 30  
163 Leu Ala Ala Ala Thr Gly Lys Gln Glu Leu Ala Lys Tyr Phe Leu Ala  
164 35 40 45  
166 Glu Leu Leu Ser Glu Pro Asn Gln Thr Glu Asn Asp Ala Leu Glu Pro  
167 50 55 60  
169 Glu Asp Leu Pro Gln Ala Ala Glu Gln Asp Glu Met Arg Leu Glu Leu  
170 65 70 75 80  
172 Gln Arg Ser Ala Asn Ser Asn Pro Ala Met Ala Pro Arg Glu Arg Lys  
173 85 90 95  
174 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys  
175 100 105 110

177 (2) INFORMATION FOR SEQ ID NO: 4:  
179 (i) SEQUENCE CHARACTERISTICS:  
180 (A) LENGTH: 427 base pairs  
181 (B) TYPE: nucleic acid  
182 (C) STRANDEDNESS: single  
183 (D) TOPOLOGY: linear  
185 (ii) MOLECULE TYPE: cDNA  
187 (iii) HYPOTHETICAL: NO  
189 (iv) ANTI-SENSE: NO  
192 (ix) FEATURE:  
193 (A) NAME/KEY: CDS  
194 (B) LOCATION: 25..354

197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
199 GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC 51  
200 Met Met Gly Gly Arg Gly Thr Gly Gly  
201 1 5  
203 AAG TGG CCC TCA GCC TTC GGG CTG CTG CTC TGG GGG GTC GCA GCC 99  
204 Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Trp Gly Val Ala Ala  
205 10 15 20 25  
207 TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG 147  
208 Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln  
209 30 35 40  
211 GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG 195  
212 Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp  
213 45 50 55  
215 CAC GAG TGG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT 243  
216 His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly  
217 60 65 70  
219 ACC CCC GGG CTG TCC AAG AGC CAG GAA AGG CCA CCC CCC CAA CAG CCC 291

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220 Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro  
221 75 80 85  
223 CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC 339  
224 Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe  
225 90 95 100 105  
226 TCC TCG TGC AAG TAACCCCACC CTGGGCATAG CACCCTGGCC ACCCTGTGAG 391  
227 Ser Ser Cys Lys

W--> 228 110

230 ATGCCAACGA GACCTGAATA AAGACTGTCA ATCAAC 427

233 (2) INFORMATION FOR SEQ ID NO: 5:

235 (i) SEQUENCE CHARACTERISTICS:

236 (A) LENGTH: 109 amino acids  
237 (B) TYPE: amino acid  
238 (D) TOPOLOGY: linear

240 (ii) MOLECULE TYPE: protein

242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

244 Met Met Gly Gly Arg Gly Thr Gly Gly Lys Trp Pro Ser Ala Phe Gly  
245 1 5 10 15

247 Leu Leu Leu Leu Trp Gly Val Ala Ala Ser Ala Leu Pro Leu Glu Ser  
248 20 25 30

250 Gly Pro Thr Gly Gln Asp Ser Val Gln Glu Ala Thr Glu Gly Arg Ser  
251 35 40 45

253 Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala Ser Gln Ala  
254 50 55 60

256 Ser Ser Ser Thr Pro Val Gly Gly Thr Pro Gly Leu Ser Lys Ser  
257 65 70 75 80

259 Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro  
260 85 90 95

262 Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
263 100 105

266 (2) INFORMATION FOR SEQ ID NO: 6:

268 (i) SEQUENCE CHARACTERISTICS:

269 (A) LENGTH: 85 amino acids  
270 (B) TYPE: amino acid  
271 (D) TOPOLOGY: linear

273 (ii) MOLECULE TYPE: protein

275 (v) FRAGMENT TYPE: C-terminal

279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

281 Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln  
282 1 5 10 15

283 Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp  
284 20 25 30

286 Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly  
287 35 40 45

289 Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln  
290 50 55 60

292 Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr  
293 65 70 75 80

295 Phe Ser Ser Cys Lys

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296 85  
298 (2) INFORMATION FOR SEQ ID NO: 7:  
300 (i) SEQUENCE CHARACTERISTICS:  
301 (A) LENGTH: 29 amino acids  
302 (B) TYPE: amino acid  
303 (D) TOPOLOGY: linear  
305 (ii) MOLECULE TYPE: protein  
307 (v) FRAGMENT TYPE: C-terminal  
311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
313 Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro  
314 1 5 10 15  
316 Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
317 20 25  
319 (2) INFORMATION FOR SEQ ID NO: 8:  
321 (i) SEQUENCE CHARACTERISTICS:  
322 (A) LENGTH: 14 amino acids  
323 (B) TYPE: amino acid  
324 (D) TOPOLOGY: linear  
326 (ii) MOLECULE TYPE: protein  
328 (v) FRAGMENT TYPE: C-terminal  
332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
334 Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
335 1 5 10  
337 (2) INFORMATION FOR SEQ ID NO: 9:  
339 (i) SEQUENCE CHARACTERISTICS:  
340 (A) LENGTH: 13 amino acids  
341 (B) TYPE: amino acid  
342 (D) TOPOLOGY: linear  
344 (ii) MOLECULE TYPE: protein  
346 (v) FRAGMENT TYPE: internal  
350 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
352 Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp  
353 1 5 10  
355 (2) INFORMATION FOR SEQ ID NO: 10:  
357 (i) SEQUENCE CHARACTERISTICS:  
358 (A) LENGTH: 84 amino acids  
359 (B) TYPE: amino acid  
360 (D) TOPOLOGY: linear  
362 (ii) MOLECULE TYPE: protein  
364 (v) FRAGMENT TYPE: C-terminal  
368 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
370 Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln  
371 1 5 10 15  
373 Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp  
374 20 25 30  
376 His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly  
377 35 40 45  
379 Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Gln Gln Pro  
380 50 55 60

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/766,396

DATE: 06/26/2001

TIME: 15:12:00

Input Set : N:\Crf3\RULE60\09766396.txt  
Output Set: N:\CRF3\06262001\I766396.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4